

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,191
Source: JFWP
Date Processed by STIC: 02/22/2007

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 02/22/2007

PATENT APPLICATION: US/10/562,191

TIME: 10:15:21

Input Set : F:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\02222007\J562191.raw

3 <110> APPLICANT: CHIRON SRL
 4 MASIGNANI, Vega
 5 ARICO, Maria Beatrice
 7 <120> TITLE OF INVENTION: Virulence-associated Adhesins
 9 <130> FILE REFERENCE: PP020667.0003
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/562,191
 C--> 12 <141> CURRENT FILING DATE: 2005-12-22
 14 <150> PRIOR APPLICATION NUMBER: GB0315022.4
 15 <151> PRIOR FILING DATE: 2003-06-26
 18 <160> NUMBER OF SEQ ID NOS: 65
 20 <170> SOFTWARE: SeqWin99, version 1.02
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 223
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Haemophilus aegyptius
 27 <400> SEQUENCE: 1
 28 Met Lys Arg Asn Leu Leu Lys Gln Ser Val Ile Ala Val Leu Ile Gly
 29 1 5 10 15
 31 Gly Thr Thr Val Ser Asn Tyr Ala Leu Ala Gln Ala Gln Ala
 32 20 25 30
 34 Gln Val Lys Lys Asp Glu Leu Ser Glu Leu Lys Lys Gln Val Lys Glu
 35 35 40 45
 37 Met Asp Ala Ala Ile Asp Gly Ile Leu Asp Asp Asn Ile Ala Tyr Glu
 38 50 55 60
 40 Ala Glu Val Asp Ala Lys Leu Asp Gln His Ser Ala Ala Leu Gly Arg
 41 65 70 75 80
 43 His Thr Asn Arg Leu Asn Asn Leu Lys Thr Ile Ala Glu Lys Ala Lys
 44 85 90 95
 46 Gly Asp Ser Ser Glu Ala Leu Asp Lys Ile Glu Ala Leu Glu Glu Gln
 47 100 105 110
 49 Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
 50 115 120 125
 52 Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
 53 130 135 140
 55 Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
 56 145 150 155 160
 58 Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
 59 165 170 175
 61 Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
 62 180 185 190
 64 Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
 65 195 200 205
 67 Ala Ala Val Gly Gly Tyr Lys Ser Gln Thr Ala Val Ala Val Gly

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```

68      210      215      220
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 338
72 <212> TYPE: PRT
73 <213> ORGANISM: Escherichia coli
75 <400> SEQUENCE: 2
76 Met Lys Thr Val Asn Val Ala Leu Leu Ala Leu Ile Ile Ser Ala Thr
77 1      5      10      15
79 Ser Ser Pro Val Leu Ala Gly Asp Thr Ile Glu Ala Ala Thr
80      20      25      30
82 Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
83      35      40      45
85 Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
86      50      55      60
88 Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
89 65      70      75      80
91 Thr Gln Thr Pro Thr Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr
92      85      90      95
94 Val Ala Ala Thr Gly Asp Val Gln Thr Thr Ala Arg Tyr Gln Ser Met
95      100     105     110
97 Ile Asn Ala Arg Gln Ser Ala Val Thr Asp Ala Gln Gln Thr Gln Ile
98      115     120     125
100 Thr Glu Gln Gln Ala Gln Ile Val Ala Thr Gln Lys Thr Leu Ala Ala
101      130     135     140
103 Thr Gly Asp Thr Gln Asn Thr Ala His Tyr Gln Glu Met Ile Asn Ala
104 145     150     155     160
106 Arg Leu Ala Ala Gln Asn Glu Ala Asn Gln Arg Thr Ala Thr Glu Gln
107      165     170     175
109 Gly Gln Lys Met Asn Ala Leu Thr Thr Asp Val Ala Val Gln Gln Gln
110      180     185     190
112 Asn Glu Arg Thr Gln Tyr Asp Lys Gln Met Gln Ser Leu Ala Gln Glu
113      195     200     205
115 Ser Ala Gln Ala His Glu Gln Ile Asp Ser Leu Ser Gln Asp Val Thr
116      210     215     220
118 Gln Thr His Gln Gln Leu Thr Asn Thr Gln Lys Arg Val Ala Asp Asn
119 225     230     235     240
121 Ser Gln Gln Ile Asn Thr Leu Asn Asn His Phe Ser Ser Leu Lys Asn
122      245     250     255
124 Glu Val Asp Asp Asn Arg Lys Glu Ala Asn Ala Gly Thr Ala Ser Ala
125      260     265     270
127 Ile Ala Ile Ala Ser Gln Pro Gln Val Lys Thr Gly Asp Val Met Met
128      275     280     285
130 Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
131      290     295     300
133 Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile
134 305     310     315     320
137 Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
138      325     330     335
140 Ser Phe

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```

143 <210> SEQ ID NO: 3
144 <211> LENGTH: 1588
145 <212> TYPE: PRT
146 <213> ORGANISM: Escherichia coli
148 <400> SEQUENCE: 3
149 Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Asn Tyr
150 1 5 10 15
152 Thr Val Thr Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
153 20 25 30
155 Ser Lys Leu Ile Ser Ala Leu Val Ala Gly Gly Met Leu Ser Ser
156 35 40 45
158 Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
159 50 55 60
161 Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
162 65 70 75 80
164 Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
165 85 90 95
167 Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
168 100 105 110
170 Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
171 115 120 125
173 Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
174 130 135 140
176 Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
177 145 150 155 160
179 Lys Leu Ser Ile Ala Met Gly Asp Ser Ser Lys Ala Glu Gly Ala Asn
180 165 170 175
182 Ala Ile Ala Leu Gly Asn Ala Thr Lys Ala Thr Glu Ile Met Ser Ile
183 180 185 190
185 Ala Leu Gly Asp Thr Ala Asn Ala Ser Lys Ala Tyr Ser Met Ala Leu
186 195 200 205
188 Gly Ala Ser Ser Val Ala Ser Glu Glu Asn Ala Ile Ala Ile Gly Ala
189 210 215 220
191 Glu Thr Glu Ala Ala Glu Asn Ala Thr Ala Ile Gly Asn Asn Ala Lys
192 225 230 235 240
194 Ala Lys Gly Thr Asn Ser Met Ala Met Gly Phe Gly Ser Leu Ala Asp
195 245 250 255
197 Lys Val Asn Thr Ile Ala Leu Gly Asn Gly Ser Gln Ala Leu Ala Asp
198 260 265 270
200 Asn Ala Ile Ala Ile Gly Gln Gly Asn Lys Ala Asp Gly Val Asp Ala
201 275 280 285
203 Ile Ala Leu Gly Asn Gly Ser Gln Ser Arg Gly Leu Asn Thr Ile Ala
204 290 295 300
206 Leu Gly Thr Ala Ser Asn Ala Thr Gly Asp Lys Ser Leu Ala Leu Gly
207 305 310 315 320
209 Ser Asn Ser Ser Ala Asn Gly Ile Asn Ser Val Ala Leu Gly Ala Asp
210 325 330 335
212 Ser Ile Ala Asp Leu Asp Asn Thr Val Ser Val Gly Asn Ser Ser Leu
213 340 345 350

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```

215 Lys Arg Lys Ile Val Asn Val Lys Asn Gly Ala Ile Lys Ser Asp Ser
216          355          360          365
218 Tyr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Ala Ile Ser Asp Ser Val
219          370          375          380
221 Ala Lys Arg Leu Gly Gly Gly Ala Ala Val Asp Val Asp Asp Gly Thr
222 385          390          395          400
224 Val Thr Ala Pro Thr Tyr Asn Leu Lys Asn Gly Ser Lys Asn Asn Val
225          405          410          415
227 Gly Ala Ala Leu Ala Val Leu Asp Glu Asn Thr Leu Gln Trp Asp Gln
228          420          425          430
230 Thr Lys Gly Lys Tyr Ser Ala Ala His Gly Thr Ser Ser Pro Thr Ala
231          435          440          445
233 Ser Val Ile Thr Asp Val Ala Asp Gly Thr Ile Ser Ala Ser Ser Lys
234          450          455          460
236 Asp Ala Val Asn Gly Ser Gln Leu Lys Ala Thr Asn Asp Asp Val Glu
237 465          470          475          480
239 Ala Asn Thr Ala Asn Ile Ala Thr Asn Thr Ser Asn Ile Ala Thr Asn
240          485          490          495
242 Thr Ala Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp
243          500          505          510
245 Ser Val Gly Asp Leu Gln Ala Asp Ala Leu Leu Trp Asn Glu Thr Lys
246          515          520          525
248 Lys Ala Phe Ser Ala Ala His Gly Gln Asp Thr Thr Ser Lys Ile Thr
249          530          535          540
251 Asn Val Lys Asp Ala Asp Leu Thr Ala Asp Ser Thr Asp Ala Val Asn
252 545          550          555          560
254 Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr
255          565          570          575
257 Asn Ile Ala Asn Asn Thr Ser Asn Ile Ala Thr Asn Thr Thr Asn Ile
258          580          585          590
260 Ser Asn Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys
261          595          600          605
263 Trp Asp Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Thr Glu Thr
264          610          615          620
266 Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser
267 625          630          635          640
269 Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val
270          645          650          655
273 Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn
274          660          665          670
276 Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp
277          675          680          685
279 Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser
280          690          695          700
282 Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp
283 705          710          715          720
285 Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr
286          725          730          735
288 Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly

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```

289          740          745          750
291 Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala
292          755          760          765
294 Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu
295          770          775          780
297 Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn
298 785          790          795          800
300 Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp
301          805          810          815
303 Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser
304          820          825          830
306 Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly
307          835          840          845
309 Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
310          850          855          860
312 Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
313 865          870          875          880
315 Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
316          885          890          895
318 Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
319          900          905          910
321 Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
322          915          920          925
324 Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
325          930          935          940
327 Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
328 945          950          955          960
330 Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
331          965          970          975
333 Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
334          980          985          990
336 His Asp Gly Lys Ala Ser Ile Ile Thr Asn Val Ala Asn Gly Ser Ile
337          995          1000          1005
339 Ser Glu Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Asn Ala Thr
340          1010          1015          1020
342 Asn Met Met Ile Glu Gln Asn Thr Gln Ile Ile Asn Gln Leu Ala Gly
343 1025          1030          1035          1040
345 Asn Thr Asp Ala Thr Tyr Ile Gln Glu Asn Gly Ala Gly Ile Asn Tyr
346          1045          1050          1055
348 Val Arg Thr Asn Asp Asp Gly Leu Ala Phe Asn Asp Ala Ser Ala Gln
349          1060          1065          1070
351 Gly Val Gly Ala Thr Ala Ile Gly Tyr Asn Ser Val Ala Lys Gly Asp
352          1075          1080          1085
354 Ser Ser Val Ala Ile Gly Gln Gly Ser Tyr Ser Asp Val Asp Thr Gly
355          1090          1095          1100
357 Ile Ala Leu Gly Ser Ser Ser Val Ser Ser Arg Val Ile Ala Lys Gly
358 1105          1110          1115          1120
360 Ser Arg Asp Thr Ser Ile Thr Glu Asn Gly Val Val Ile Gly Tyr Asp
361          1125          1130          1135

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/562,191DATE: 02/22/2007
TIME: 10:15:22Input Set : F:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\02222007\J562191.raw**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 787
Seq#:29; N Pos. 2359
Seq#:39; Xaa Pos. 2,3,6,7,9,10,14,17,19,22,28,30,32,33,34,40,41,43,45,47,49
Seq#:39; Xaa Pos. 50,51,53,54,55,56,57,58,59,60,61,62,63,64,65,66,69,71,73
Seq#:39; Xaa Pos. 74,75,76,79,85,91,92,93,94,95,96,100,102,103,104,105,106
Seq#:39; Xaa Pos. 118,119,120,123,127,128,130,131,132,138,147,152,153,154
Seq#:39; Xaa Pos. 155,156,158,159,161,162,164,166,168,211,213,214,215,217
Seq#:39; Xaa Pos. 219,223,224,232,234,237,238,240,241,244,245,247,248,250
Seq#:39; Xaa Pos. 251,252,253,254,257,258,259,260,261,263,264,265,267,268
Seq#:39; Xaa Pos. 272,273,274,275,276,277,278,279,280,281,282,283,284,287
Seq#:39; Xaa Pos. 289,291,297,299,301,304,306,309,310,311,312,313,314,315
Seq#:39; Xaa Pos. 316,317,318,319,320,321,322,323,324,325,326,328,334,335
Seq#:39; Xaa Pos. 337,339,340,341,343,344,345,349,350,353,355,356,361,363
Seq#:39; Xaa Pos. 364,367,368,369,370,372,373,375,376,378,383,385,389,392
Seq#:39; Xaa Pos. 394,395,402,409,414,446,448,449,451,455,458,464,472,476
Seq#:39; Xaa Pos. 484

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:39; Line(s) 4998,4999,5000

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3011 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:3164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:784
L:4309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:4353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:2340
L:4997 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:5004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
M:341 Repeated in SeqNo=39